

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2000, 09:57:10 ; Search time 1721.35 Seconds
[without alignments]
13243.098 Million cell updates/sec

Title: US-09-117-447-1
Perfect score: 3687
Sequence: 1 atgataagaaagaaagctg.....ttacatctatattaagtaa 3687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
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116: gb_gss17:*

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 119: em-gss13:*
 120: gb-gss20:*
 121: gb-gss21:*
 122: gb-gss22:*
 123: gb-gss23:*
 124: gb-gss24:*
 125: em-gss14:*
 126: em-gss15:*
 127: em-gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	59.8	1.6	997	121	CNS0134P	AL102403 Drosophila
C 2	56.4	1.5	476	34	BE224646	BE224646 kp59a06.y
C 3	55.8	1.5	1159	121	CNS015XR	AL106041 Drosophila
C 4	55.4	1.5	773	122	CNS01VYG	AL169549 Tetraodon
C 5	55.2	1.5	735	123	CNS04NSM	AL299119 Tetraodon
C 6	55.2	1.5	917	121	CNS017SL	AL108447 Drosophila
C 7	54.2	1.5	1076	124	CNS05HXM	AL338180 Tetraodon
C 8	53.4	1.4	560	121	CNS00C13	AL059106 Drosophila
C 9	53.4	1.4	1101	121	CNS01B07	AL108721 Drosophila
C 10	53	1.4	1025	121	CNS014U2	AL104216 Drosophila
C 11	53	1.4	1147	118	BL3042	BL3042 T30M24-Sp6
C 12	51.8	1.4	959	121	CNS00655	AL062806 Drosophila
C 13	51.8	1.4	969	121	CNS00IDL	AL073848 Drosophila
C 14	51.8	1.4	1101	121	CNS00HXS	AL073856 Drosophila
C 15	51.6	1.4	470	124	FR0018463	AL011359 F. rubripes
C 16	51	1.4	1042	121	CNS0148K	AL103838 Drosophila
C 17	51	1.4	1184	123	CNS04P4P	AL300850 Tetraodon
C 18	50.8	1.4	1101	121	CNS0039G	AL063921 Drosophila
C 19	50.6	1.4	539	21	AW329517	AW329517 N200762e
C 20	50.6	1.4	1101	121	CNS00EVL	AL069706 Drosophila
C 21	49.8	1.4	989	122	CNS02H44	AL197365 Tetraodon
C 22	49.6	1.3	828	121	CNS011TX	AL100719 Drosophila
C 23	49.4	1.3	581	122	CNS034DK	AL27297 Tetraodon
C 24	49.2	1.3	809	121	CNS00A7H	AL054820 Drosophila
C 25	49	1.3	869	121	CNS00ZEX	AL097574 Drosophila
C 26	49	1.3	1223	118	BL2981	BL2981 T24D11-Sp6
C 27	48.8	1.3	1079	122	CNS035IX	AL128786 Tetraodon
C 28	48.6	1.3	1007	121	CNS00UOV	AL076752 Drosophila
C 29	48.4	1.3	421	115	AZ113646	AZ113646 RPI-23-4
C 30	48.4	1.3	443	124	FR0008252	292062 F. rubripes
C 31	48.4	1.3	450	124	FR0025683	AL018519 F. rubripes
C 32	48.4	1.3	1101	121	CNS001FB	AL060732 Drosophila
C 33	48.2	1.3	567	124	FR0006951	290761 F. rubripes
C 34	48	1.3	426	14	AL366543	AL366543 MCB80F05
C 35	48	1.3	500	20	AW126318	AW126318 N100425e
C 36	48	1.3	34	BE239628	BE239628 EST403677	
C 37	47.8	1.3	907	122	CNS021J4	AL176953 Tetraodon
C 38	47.8	1.3	1101	121	CNS01B2P	AL108811 Drosophila
C 39	47.6	1.3	945	121	CNS006WM	AL066018 Drosophila
C 40	47.4	1.3	838	123	CNS03W9J	AL264440 Tetraodon
C 41	47.2	1.3	767	121	CNS00AIX	AL055924 Drosophila
C 42	47.2	1.3	783	121	CNS00AIX	AL055833 Drosophila
C 43	47.2	1.3	823	121	CNS0105K	AL098516 Drosophila
C 44	47.2	1.3	894	34	BE215315	BE215315 HV_CEB000
C 45	47.2	1.3	1152	122	CNS024NL	AL181002 Tetraodon

ALIGNMENTS

RESULT 1
 CNS0134P/c

LOCUS	CNS0134P	997 bp	DNA	GSS	26-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence sp6 end of BAC BAC09C07 of DrosBAC library from Drosophila melanogaster (fruit fly) genomic survey sequence.				
ACCESSION	AL102403				
VERSION	AL102403.1	GI:5614014			
KEYWORDS	GSS.				
SOURCE	fruit fly.				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 997)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage; BP 191 91006 Evry cedex - FRANCE (E-mail: seqrefgenoscope.cns.fr)				
COMMENT	<p>- Web : www.genoscope.cns.fr</p> <p>Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CSH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.</p>				
FEATURES	<p>source</p> <p>1..997</p> <p>/organism="Drosophila melanogaster"</p> <p>/plasmid="pBelobAC11"</p> <p>/db_xref="taxon:7227"</p> <p>/clone_1lb="DrosBAC"</p> <p>/clone="BAC09C07"</p> <p>/note="end : sp6"</p>				
BASE COUNT	162 a	115 c	79 g	517 t	124 others
ORIGIN					
Query Match	1.6%	Score 59.8;	DB 121;	Length 997;	
Best local similarity	37.5%	Pred. No. 0.0015;			
Matches 245;	Conservative 43;	Mismatches 362;	Indels 3;	Gaps 1;	
437	aagcaaatgattgaagaaagcagaacatactatcacaaatctcttaagaaataa	496			
DB	656 AAAAAAAAAAAAAAAAAAATAAAGAAAGAAATTAAGATTGAGAAAAAAAT	597			
QY	ctcgcagctatctttagctgcgtatagttaaacacaactcgtgattactctcta	556			
DB	596 ATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	537			
QY	cattnaagcaaaagcagaactcgcagcagcttaattgatattacccgttcaa	616			
DB	536 WAAWAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	477			
QY	617 tgaagcgcgcgaagctacagacgcgtgtgaagcagcgcaattgacaaagctga	675			
DB	476 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	417			
QY	677 cgtgattcaatcatcatcatcatcaacaaagtaacagatgcttcaaatgaa	736			
DB	416 WTGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	357			
QY	737 cagaagctagcgaagaaagcagatgcagctgaagctgcgttactcgaagtgaa	795			
DB	356 AAGAAARAAARAAARAAARAAARAAARAAARAAARAAARAAARAAARAA	297			
QY	797 ggttaagtcgataacacacacacacacacacacacacacacacacacac	856			
DB	296 AAAAAARAAARAAARAAARAAARAAARAAARAAARAAARAAARAAARAA	237			
QY	857 gaacctaataattacacattcagctgcgtcgaatgaagatcagtaacgtta	916			
DB	236 NNCGANN	178			

[illegible]

DB	218	AAACAAAGTGGCGAATAAGAAAGTTGTCAAAAAAACAAGTTGCCAAAAAAGCTGTAGCACT	277
QY	1651	gaaagaagatctgtgtacagctgtgtctctctgtgactcaaatatataagcagaagcttaaatg	1710
DB	278	AAAAAAGCAACGATTCATAAGAAAGACTACTGTATGTCAAAAAATCTGCGATGTAAAAA	337
QY	1711	gtaaacttagtgcccaaaagcgcgaacttaagaagaatatacaatctatcaatcaaatlaa	1770
DB	338	ACAACTTAAGTCTCCAAAAGCTAAGACTACAGAAAAAAAAGTCTTCAAAAAACAATTGA	397
QY	1771	aaagcttgaagtcgcgaataaagtagtaattagtcgactgttaacgaagaaca	1824
DB	398	AAGAAACAAAAATCACTCTCAAAAAAGAAAGTAGCCACAAAAGTGTAAAAA	451
RESULT	3		
CNS015XR			
LOCUS			
DEFINITION	CNS015XR: 1159 bp DNA GSS 26-JUL-1999		
ACCESSION	Drosophila melanogaster genome survey sequence T7 end of BAC		
VERSION	BA001017 of DrosBAC library from Drosophila melanogaster (fruit		
KEYWORDS	fly), genomic survey sequence.		
SOURCE	Al106041		
ORGANISM	ALI06041.1 GI:5619746		
REFERENCE	GSS.		
AUTHORS	fruit fly,		
TITLE	Drosophila melanogaster.		
JOURNAL	Euarystota; Melarosa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1159)		
COMMENT	Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.egp.ebl.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.		
FEATURES			
source	Location/Qualifiers 1..1159 /organism="Drosophila melanogaster" /plasmid="pBelobAC11" /db_xref="taxon:7227" /clone_lib="DrosBAC" /clone="BA001017" /note="end : 77"		
BASE COUNT	448 a 36 c 7 g 178 t 490 others		
ORIGIN			
Query Match	1.5%, Score 55.8; DB 121; Length 1159;		
Best Local Similarity	33.8%; Pred. No. 0.013;		
Matches 189; Conservative	6; Mismatches 365; Indels 0; Gaps 0;		
QY	212	aatacaaaagcgaataaagataacgctgtagcggtgctgcatgtgaataagcaggtg	271
DB	31	AAAAAAAAAAAAAAAAAAAAAAYAAAAAACSAAAAAAAAAAANCYMAAAAAAAAAA	90
QY	272	gcgcgaataaagcagcttacttagctgattcaaaaagaatagaacttcgctttca	331
DB	91	AAACAAATAAANNNNNNNNTTNNNTTNTTAAATAAATAAATAAATAAATAAATAA	150
QY	332	aagcaaaccttaaatctgagcagagctcgtgtagcaacttaacatgacttaacatg	391
DB	151	AAAAAAAAACACCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	210
QY	392	caacaaatttgacgaatctgcgcgaagcctagaggtcgtcttcaagcaaaagttag	451

AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesnes,C., Wincker,P., Brotier,P., Queller,F., Saurin,W. and Weissbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1076)

AUTHORS Genoscope.

JOURNAL Direct Submission

COMMENT Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases. This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetradon>.

FEATURES Location/Qualifiers

source 1..1076

organism="Tetradon nigroviridis"

db_xref="taxon:99883"

clone_11b="A"

clone_11d="A"

/note="Genoscope sequence ID : CONA014CC02A1-end : T3"

BASE COUNT 160 a 260 c 309 g 333 t 14 others

ORIGIN

Query Match 1.5%; Score 54.2; DB 124; Length 1076;

Best Local Similarity 53.0%; Pred. No. 0.03;

Matches 116; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 1463 cgtgtgtaacgcctcactacttagtggtacaaactatctctgtctcttaaca 1522

Db 793 CTGTGCTACCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 852

QY 1523 caaatgttggtggttaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1582

Db 833 CTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912

QY 1583 ttcattacacacacacgtttgtctactaagttagacgaatcatttagctgtgaa 1642

Db 913 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972

QY 1643 tattagtgtgaaagaatctgtgtacagctgtgtctctg 1681

Db 973 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011

RESULT 8

CNS00C13 560 bp DNA GSS 04-JUN-1999

LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #

DEFINITION BACR25J05 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL059106

VERSION AL059106.1 GI:4946756

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 560)

AUTHORS Genoscope.

JOURNAL Direct Submission

COMMENT Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila genome project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamonoset in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES Location/Qualifiers

source 1..560

organism="Drosophila melanogaster"

db_xref="taxon:7227"

clone_11b="RPCT-98"

clone="BACR25J05"

/note="end : T7"

BASE COUNT 235 a 14 c 16 g 24 t 271 others

ORIGIN

Query Match 1.4%; Score 53.4; DB 121; Length 560;

Best Local Similarity 32.1%; Pred. No. 0.04;

Matches 120; Conservative 12; Mismatches 242; Indels 0; Gaps 0;

QY 105 aacagtagtaagcccaagaagccagttcaaaaagcatctattactaacgcatcac 164

Db 2 AARAAAR 61

QY 165 agtaacgggaactgtgtgattcccaacattacgagtgtatgtgtgatacaagaac 224

Db 62 ANNN 121

QY 225 gaaaaaacgataccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 284

Db 122 AAAAAAAR 181

QY 285 cgtctacttgctgtgtttacaaaagaatagaaactacgtttcaagaacacccaa 344

Db 182 GAAAAAAR 241

QY 345 atctgacgaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 404

Db 242 NNAAN 301

QY 405 cgaatgcgcacagagcagagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 464

Db 302 NNAAN 361

QY 465 atactatcaataa 478

Db 362 NNAAN 375

RESULT 9

CNS01807/c 1101 bp DNA GSS 26-JUL-1999

LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC

DEFINITION BACN37F07 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL108721

VERSION AL108721.1 GI:5629025

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

AUTHORS Genoscope.

JOURNAL Direct Submission

COMMENT Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (EDGP) <http://www.edgp.ebi.ac.uk>. This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billand at CERN (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES

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/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_1lib="DrosBAC"
/clone="BACN37E07"
/note="end : Sp6"
BASE COUNT      179 a      70 c      85 g      448 t      319 others
ORIGIN

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Query Match	1.48	Score 53.4	DB 121	Length 1101
Best Local Similarity	39.58	Pred. No. 0.047		
Matches 189; Conservative	20	Mismatches 269;	Indels 0;	Gaps 0

OY	635	nagcgcgttggaagaacgcgcaattttagacaacctaactgctgttgatccaatacatc	694
Db	588	AAAAAAGCTTAAAAAAAATAAAATTAATAATTTAAAAATTTAAAAAAAATAAAAA	529
OY	695	aatactaccacaagaatacagatgctttccaaactgaactaacagaaagtaacgaaaag	754
Db	528	AAATATAAAAAAAACAAAAAAAATAATTAATAAAAAATAAAATAAAATAATTAATAA	469
OY	755	catttgttcagatgaagcggcgtctctccaaaagtgaagtgtaagtgcattaca	814
Db	468	AAATAAAATWAAA	409
OY	815	ctcaacaacaagctgttgaattacagcagtaacagtgcaacgcaacctcaaatc	874
Db	408	AMAAAAAAAATAAAATTAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA	349
OY	875	tttcacgtctgccaatgaaatgaatagtaacgtaaatctgtatcgtattcataaagt	934
Db	348	WAAAAAAWWAAAAATTAATTAATAAAAAATAATTAATAAAAAATTAAATATCAANNCCANT	289
OY	935	acggttaacattccattgccccttaatacgcgcagatgctttctatctcaacgcgaaaa	994
Db	288	CTTCNCNANCTCCCAATCATCAATATWTATTAATTAATTAATTTNNNAATATAAAAAAA	229
OY	995	ctatcacctgtgatgcttcaaactccattcgaaataataacgagatataaagtatg	1055
Db	228	ATAATTAATTAATTAATAAAATAAAATAAAATAAAATAATNNANNNTAAATTATCTTAANNA	169
OY	1055	aaggatttaaagcaaaaatgycgaagaatttaagaagatgcatacattcaagct	1112
Db	168	MMAATATNNNAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAATTAATAANT	111

RESULT 10
CNS0147/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

CNS0147 1025 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BAC1111 of DrosBac library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL104216
GI:5615827
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscophora; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1025)
Genoscope.
Direct Submission

JOURNAL

JOURNAL	COMMENT
Submitted4 (23-JUL-1999) Genoscope - Centre National de Sequençage : BP 191 51006 EVRY cedex - FRANCE (E-mail : seque4@genoscope.cns.fr Web : www.genoscope.cns.fr)	Determination of this BAC-end sequence was carried out as part of a

FEATURES

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/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN11L11"
/note="end : T7"
BASE COUNT      148 a      88 c      6 g      522 t      261 others
ORIGIN

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Query Match      1.4%  Score 53:  DB 121;  Length 1025;
Best Local Similarity 33.0%  Pred. NC. 0.057;
Matches 223;  Conservative 68;  Mismatches 384;  Indels 0;  Gaps 0

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QY	226	aaataagatcacctgtgtgtagcattagtaataaagaacgggtggtcggaataaaagac	285
Db	794	AAAAAAAAAAAAAAGTCGAAAAAAAKRTTTRTGTGTAAAAAATATGTGTGRTAAKWTAA	733
QY	286	gcttacttaagtgtattacaaaagaatatgaactgaactgctttcaagaacacctaa	345
Db	734	WATRTKKGTGATGRTAARAAWAAAAATATAATAAWVGAATGCAAAAAAARAAAAA	675
QY	346	tcgtgcaagctcgtagtagcaacttaactgaatgcttacacactatgacacaaattgac	405
Db	674	ATGTRAAWMTAAWTTTKKATTTGTGAATTGCTTGCTKAAABAAAAAABAAAAAARKMT	613
QY	406	gaatagcgcaagacagacagagcgctgtgttcaagcaaaagattgaanaagacagaa	465
Db	614	AAWKKTAARAADGKTWKTKRTTTRAAWAAAGGTCGAKAGTTRDWAAAAAATAAAA	555
QY	466	tactatcacaaatccttatgaatataaacaactcgacagtcattttaagtcggtat	525
Db	554	AAAAAAAAAAAAAGTCGAADARAAADARADAGKAAAAARKRTATKGTGKTK	495
QY	526	ggtaaacaactgcgtgatttacttcgcctacatttaagcaaaagcacagaacttcgc	585
Db	494	TGTTATGTAAJAKWATWAAAGTGTCKKMTATATAAAAAABAAAAAANKRTG	435
QY	586	gacgcgttaatttatgatattacocgtgtgcaatgaagcgcgagatcaagaagctgtg	645
Db	434	GRTKRRGAATTTAATRTAKKTTAAAAAATAATGTWTTATKTKTGKTCDDKARAADAAAT	375
QY	646	aaagcagcgcaatttagacaagaagcgaagcgctgtgtatcaaatcaaatgaacttcca	705
Db	374	TAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	315
QY	706	aaagtacaagttgctttcaaaactgaaactaaagaagtgcgaataaaagcatatagatga	765
Db	314	AAAAAAAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	255
QY	766	gatgaagctgcttacttccaaaagtgtgaagtgtaagtgcgatttaactcacaacaaa	825
Db	254	AAAAAAAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	195
QY	826	gctgtgaattaaacagcagtcaccagtgaaacgagacctaanaattacaacttcagctgc	885
Db	194	AAAAAAAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	135
QY	886	gcgaatgaagatataca 900	


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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1ib="RPC1-98"
/clone="BACR36C06"
/note="end : TET3"
BASE COUNT      525 a      63 c      52 g      106 t      213 others
ORIGIN

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Query Match      1.4%; Score 51.8; DB 121; Length 959;
Best Local Similarity 32.8%; Pred. No. 0.11;
Matches 167; Conservative 80; Mismatches 262; Indels 0; Gaps 0;

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OY 437 aagcaaaagatttagaagaagcagaacaatactatcacaaatctccttaagaattaa 496
    |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 AAAAAAAAAAAAAAAAAAAAAAAAAAACAACCAAAAAAAAAAAAAAAAAAAAAA 352

OY 497 ctgcacagctcatttagatcggtatagttaaacacactcgatttacttcgctta 556
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 353 CACACANAWYTAATAAACACGCSMYNMAAMMAAMCMAAGRTTSTSCWTCGCC 412

OY 557 catttaagcaaaagcagaacactcgacagcttaatttatgatattaccgttgca 616
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 413 CCCCMCCCCSARARARARARARARARARARARARARARARARARARARAR 472

OY 617 tgaagcgcgcagtagaagacgcgtgtgaagcagcgaatttagaacaagcgaagctc 676
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 473 GAKAKARARARARARARARARARARARARARARARARARARARARARARAR 532

OY 677 ctgtgatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 736
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 533 GRARARARARARARARARARARARARARARARARARARARARARARARARAR 592

OY 737 cagaagtagcgaagaagcatttagatcggtatagttaaacacactcgatttacttcgctta 796
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 593 KMAAARARARARARARARARARARARARARARARARARARARARARARARAR 652

OY 797 gctgaagtcgatttaacacacacacacacacacacacacacacacacacacacac 856
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 653 AATATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 712

OY 857 gaacataaattcaacacttcagctgcgtcgaatgaagatacagaacagtaactag 916
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 713 AAAAAARARARARARARARARARARARARARARARARARARARARARARARAR 772

OY 917 taagtattcattatgaagtcgaagcgaact 945
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 773 AADGARRGDTDAAMARARARARARARARARARARARARARARARARARARAR 801

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RESULT 13
CNS00IDL 969 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR36C06 of RPC1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL074848
VERSION AL074848.1 GI:4954426
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
          Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
          I (bases 1 to 969)
REFERENCE Direct Submission
AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL bp 191.91006 evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - web : www.genoscope.cns.fr)
          Determination of this BAC-end sequence was carried out as part of a
          collaboration with the Berkeley Drosophila Genome Project (BDGP).
          The BDGP is constructing a physical map of the Drosophila

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melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammone in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

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1..969
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1ib="RPC1-98"
/clone="BACR36C06"
/note="end : TET3"

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BASE COUNT      502 a      133 c      93 g      150 t      91 others
ORIGIN

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Query Match      1.4%; Score 51.8; DB 121; Length 969;
Best Local Similarity 40.5%; Pred. No. 0.11;
Matches 158; Conservative 27; Mismatches 205; Indels 0; Gaps 0;

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OY 190 aacattacgattatatactctgaatacaacaagcgaataaacgatacgtatcgctga 249
    |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 43 AACARARARARARARARARARARARARARARARARARARARARARARARARAR 102

OY 250 gcatatgaataaagcagtgcgcaaaagacgcttacttagctgatttacaaga 309
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 103 CAACCGAARARARARARARARARARARARARARARARARARARARARARARAR 162

OY 310 gaattgaacttactgttttcaagaaccccttaacttcggtgaagctgtgtgaagc 369
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 163 CAARARARARARARARARARARARARARARARARARARARARARARARARAR 222

OY 370 taactgaatgcttacaactcgaacaaatgaagcaatggcgaagcgaagcgaagcgt 429
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 AAAAAARARARARARARARARARARARARARARARARARARARARARARARAR 282

OY 430 gctgtcagaagaagatttagaagaagcagaacatactatcacaagaattccttaga 489
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 283 MACACARARARARARARARARARARARARARARARARARARARARARARARAR 342

OY 490 attaaactgcacagctcatttagatcggtatagttaaacacacactcggtgattact 549
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 343 AAAAAARARARARARARARARARARARARARARARARARARARARARARARAR 402

OY 550 cgcctcatttaagcaaaagcagaaga 579
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 403 GCCGAARARARARARARARARARARARARARARARARARARARARARARARAR 432

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RESULT 14
CNS00HX9 1101 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR35M04 of RPC1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL073856
VERSION AL073856.1 GI:4953938
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
          Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
          I (bases 1 to 1101)
REFERENCE Direct Submission
AUTHORS

```

The BDGP is constructing a physical map of the Drosophila

JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr) - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bdgpc.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1.1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPci-98"
/clone="BACR35M04"
/note="end : TET3"

BASE COUNT 164 a 100 c 120 g 616 t 101 others

ORIGIN

Query Match 1.48; Score 51.8; DB 121; Length 1101;
Best Local Similarity 40.18; Pred. No. 0.11;
Matches 241; Conservative 32; Mismatches 324; Indels 4; Gaps 1;

258 gaaataagcagcggcgccgaagaagcgttacttgcgattacaaagaatcga 317
618 GAAGCTAAGCGAGATCAAAATAAAATAAAATAAAATAAAATAAAATAAA 559
318 aacttcgcttcaagcaaccctaaatcgcgaagctcgtctagcaacttacc 377
558 AAGTAAATAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 499
378 tgcctcaactatgcacaaattgacgaatgcgcgaagcctgagcgtcttca 437
498 AAATATATATATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 439
438 agcaaaagattagaaagcgaacatactacacaaatccctgaagaattaaac 497
438 TGTAAAGAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 379
498 tcgcacagtcatttcgacgcgtatcgttaaacacacacgcgtatttact 557
378 ----AAATAATAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 323
558 atttaagcaaaagcacaagcactcgcgcagccttaattatgataatccg 617
322 AAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 263
618 gaaagcgcgcgaagctacagcgtctgaaagcagcgaattagaaagctaa 677
262 AAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 203
678 tctgtatcaaatcaatcaatcaatcaatcaatcaatcaatcaatcaatca 737
202 TWTAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 143
738 aggaagtagcgaagaagcattagatcgcagatgagcgtcctactcacaag 797
142 AATAGTAAATGAGTAAATAAAATAAAATAAAATAAAATAAAATAAAATA 83
798 tctgaagtgagattacaactcaaaacaaagcgttgatattacgcggttacc 857
82 TAAATATTTTCAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 23

QY 858 a 858
Db 22 A 22

RESULT 15

FR018463/c
LOCUS FR018463 470 bp DNA GSS 09-DEC-1997
DEFINITION F. rubripes GSS sequence, clone 016E10aC6, genomic survey sequence.
ACCESSION AL011359
VERSION AL011359.1 GI:2676793
KEYWORDS GSS: genome survey sequence.
SOURCE Fugu rubripes.
ORGANISM Fugu rubripes.

REFERENCE 1 (bases 1 to 470)
Eliger,G., Clark,M., Smith,S., Week,S., Warner,S., Umranta,Y., Williams,G. and Brenner,S.
AUTHORS

TITLE

JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biobhelphgmp.mrc.ac.uk

Vector: pBluescript II KS
V-type: phagemid
PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic

FEATURES

source
1.470
/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 016E10"
/clone="016E10aC6"

BASE COUNT 149 a 79 c 150 g 65 t 27 others

ORIGIN

Query Match 1.48; Score 51.6; DB 124; Length 470;
Best Local Similarity 44.98; Pred. No. 0.1;
Matches 159; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 1264 gttaactatcacagatgttbaaactggaagaagcattccaglaattgcatctactt 1323
Db 396 GCTGCTACTACTGCTGCTGCTACTACTGCTGCTACTACTACTACTACTACTACT 337
QY 1324 tctacaactactatcgttbaaagaagcgttaagtaactggttaacaataacttgc 1383
Db 336 GCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTACTACTACTACT 277
QY 1384 atcaataagttaaacattaaacttgcgttcaatgcaagaagccttaagctagttac 1443
Db 276 GCTACTGCTACTGCTGCTGCTACTACTGCTACTGCTACTGCTGCTGCTGCTGCT 217
QY 1444 gcaaaagcattccagcaacacgttgctacacgcctcctactactttaggtgtacaatt 1503
Db 216 NCTNCTGCTACTGCTGCTGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 157
QY 1504 tctactggttcttctacaacaaatgtttggggttaatttgcgtggtggtggtgaagct 1563
Db 156 GCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 97
QY 1564 ggaactattatccttggttcttcaatccaaacaagcttgcctactaagttagac 1617
Db 96 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43

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